

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/528,709A
Source: FWO
Date Processed by STIC: 10/4/06

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 10/04/2006

PATENT APPLICATION: US/10/528,709A

TIME: 11:45:28

Input Set : A:\sequencelisting.txt

Output Set: N:\CRF4\10042006\J528709A.raw

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4 <110> APPLICANT: Geiser, Martin
5      Geisse, Sabine
6      Ostemeier, Christian
7      Ramage, Paul
8      Raulf, Friedrich
9      Zenke, Gerhard
11 <120> TITLE OF INVENTION: Three-Dimensional Structure of the
12      Catalytic Domain of ZAP-70 Protein Tyrosine Kinase, Methods
13      and Use Thereof
15 <130> FILE REFERENCE: 4-32688
17 <140> CURRENT APPLICATION NUMBER: US 10/528,709A
18 <141> CURRENT FILING DATE: 2005-03-22
20 <150> PRIOR APPLICATION NUMBER: PCT/EP03/10686
21 <151> PRIOR FILING DATE: 2003-09-25
23 <150> PRIOR APPLICATION NUMBER: US 60/413,704
24 <151> PRIOR FILING DATE: 2002-09-26
26 <160> NUMBER OF SEQ ID NOS: 6
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 619
32 <212> TYPE: PRT
33 <213> ORGANISM: Homo sapiens
35 <400> SEQUENCE: 1
36 Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
37 1          5          10          15
38 Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
39          20          25          30
40 Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
41          35          40          45
42 Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
43          50          55          60
44 Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
45 65          70          75          80
46 Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
47          85          90          95
48 Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
49          100         105         110
50 Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
51          115         120         125
52 Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
53          130         135         140
54 Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
55 145         150         155         160

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56 Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
57          165          170          175
58 Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg
59          180          185          190
60 Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val
61          195          200          205
62 Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
63          210          215          220
64 Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys
65 225          230          235          240
66 Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn
67          245          250          255
68 Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala
69          260          265          270
70 His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn
71          275          280          285
72 Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys
73          290          295          300
74 Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser
75 305          310          315          320
76 Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn
77          325          330          335
78 Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val
79          340          345          350
80 Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile
81          355          360          365
82 Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met
83          370          375          380
84 Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg
85 385          390          395          400
86 Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met
87          405          410          415
88 Ala Gly Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu
89          420          425          430
90 Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly
91          435          440          445
92 Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala
93          450          455          460
94 Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe
95 465          470          475          480
96 Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg
97          485          490          495
98 Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn
99          500          505          510
100 Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr
101          515          520          525
102 Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys
103          530          535          540
104 Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys

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```

105 545                               550                               555                               560
106 Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp
107                               565                               570                               575
108 Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg
109                               580                               585                               590
110 Met Arg Ala Cys Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro
111                               595                               600                               605
112 Gly Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala
113      610                               615
116 <210> SEQ ID NO: 2
117 <211> LENGTH: 322
118 <212> TYPE: PRT
119 <213> ORGANISM: Homo sapiens
121 <400> SEQUENCE: 2
122 Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met Pro Met Asp Thr Ser
123 1      5      10      15
124 Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu Leu Lys Asp Lys Lys
125      20      25      30
126 Leu Phe Leu Lys Arg Asp Asp Leu Leu Ile Ala Asp Ile Glu Leu Gly
127      35      40      45
128 Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val Tyr Arg Met Arg Lys
129      50      55      60
130 Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys Gln Gly Thr Glu Lys
131 65      70      75      80
132 Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln Ile Met His Gln Leu
133      85      90      95
134 Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val Cys Gln Ala Glu Ala
135      100     105     110
136 Leu Met Leu Val Met Glu Met Ala Gly Gly Gly Pro Leu His Lys Phe
137      115     120     125
138 Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser Asn Val Ala Glu Leu
139      130     135     140
140 Leu His Gln Val Ser Met Gly Met Lys Tyr Leu Glu Glu Lys Asn Phe
141 145     150     155     160
142 Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Val Asn Arg His
143      165     170     175
144 Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys Ala Leu Gly Ala Asp
145      180     185     190
146 Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys Trp Pro Leu Lys Trp
147      195     200     205
148 Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe Ser Ser Arg Ser Asp
149      210     215     220
150 Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala Leu Ser Tyr Gly Gln
151 225     230     235     240
152 Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val Met Ala Phe Ile Glu
153      245     250     255
154 Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys Pro Pro Glu Leu Tyr
155      260     265     270
156 Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp Glu Asp Arg Pro Asp

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157          275          280          285
158 Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys Tyr Tyr Ser Leu Ala
159          290          295          300
160 Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln Lys Ala Glu Ala Ala
161 305          310          315          320
162 Cys Ala
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 74
168 <212> TYPE: DNA
169 <213> ORGANISM: Unknown
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Oligo MG474
174 <400> SEQUENCE: 3
175 cagatggata cacccttgag ccagcactgg aagttctgtt ccaggggccc cgcataacgt 60
176 cccagacaa accg 74
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 20
180 <212> TYPE: DNA
181 <213> ORGANISM: Unknown
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Oligo RS366
186 <400> SEQUENCE: 4
187 acaacgcaca gaatctagcg 20
189 <210> SEQ ID NO: 5
190 <211> LENGTH: 74
191 <212> TYPE: DNA
192 <213> ORGANISM: Unknown
194 <220> FEATURE:
195 <223> OTHER INFORMATION: Oligo MG475
197 <400> SEQUENCE: 5
198 cacactccca gccacccat ccacgctgga agttctgttc caggggccct tgactcatcc 60
199 tcagagacga atcg 74
201 <210> SEQ ID NO: 6
202 <211> LENGTH: 57
203 <212> TYPE: DNA
204 <213> ORGANISM: Unknown
206 <220> FEATURE:
207 <223> OTHER INFORMATION: Oligo MG479
209 <400> SEQUENCE: 6
210 gctcgaattc tcaatgatga tgatgatgat gggcacaggc agcctcagcc ttctgtg 57

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VERIFICATION SUMMARY

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Input Set : A:\sequencelisting.txt

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